

# SEQUENCE LISTING

<110> Negulescu, Paul  
Offermanns, Stefan  
Simon, Melvin  
Zuker, Charles

<120> PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE

<130> 08366/002001

<140> US 08/878,801

<141> 1997-06-19

<150> US 60/020,234

<151> 1996-06-21

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1125

<212> DNA

<213> Mus musculus

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<221> CDS

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gat gag aag gcc gcc gcc cgg gtg gac cag gag atc aac agg atc ctc	96
Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu	
20 25 30	
ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg	144
Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu	
35 40 45	
ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc	192
Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile	
50 55 60	
atc cac ggc gcc gcc tac tcg gag gag gag cgc aag ggc ttc cgg ccc	240
Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro	
65 70 75 80	
ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc	288
Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala	
85 90 95	
atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac	336
Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His	
100 105 110	
gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag	384
Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu	
115 120 125	
aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc	432
Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile	
130 135 140	

cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala 145 150 155 160	480
gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val 165 170 175	528
ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile 180 185 190	576
aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp 195 200 205	624
gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu 210 215 220	672
aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln 225 230 235 240	720
tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala 245 250 255	768
ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val 260 265 270	816
atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr 275 280 285	864
tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp 290 295 300	912
gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr 305 310 315 320	960
acc ggg tgc gtg gac ggc ccc gag ggc agc aag aag ggc gca cga tcc Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser 325 330 335	1008
cga cgc ctt ttc agc cac tac aca tgt gcc aca gac aca cag aac atc Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile 340 345 350	1056
cgc aag gtc ttc aag gac gtg cgg gac tcg gtg ctc gcc cgc tac ctg Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu 355 360 365	1104
gac gag atc aac ctg ctg tga Asp Glu Ile Asn Leu Leu 370	1125

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 35 40 45  
 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile  
 50 55 60  
 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro  
 65 70 75 80  
 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala  
 85 90 95  
 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His  
 100 105 110  
 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu  
 115 120 125  
 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile  
 130 135 140  
 Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala  
 145 150 155 160  
 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val  
 165 170 175  
 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile  
 180 185 190  
 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp  
 195 200 205  
 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu  
 210 215 220  
 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln  
 225 230 235 240  
 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala  
 245 250 255  
 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val  
 260 265 270  
 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr  
 275 280 285  
 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp  
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 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr  
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 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser  
 325 330 335  
 Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile  
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 Asp Glu Ile Asn Leu Leu  
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 <212> DNA  
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 gag gag aag act gcc gcc aga atc gac cag gag atc aac agg att ttg  
 Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu  
 20 25 30

48

96

ttg gaa cag aaa aaa caa gag cgc gag gaa ttg aaa ctc ctg ctg ttg Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu	144
35 40 45	
ggg cct ggt gag agc ggg aag agt acg ttc atc aag cag atg cgc atc Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile	192
50 55 60	
att cac ggt gtg ggc tac tcg gag gag gac cgc aga gcc ttc cgg ctg Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu	240
65 70 75 80	
ctc atc tac cag aac atc ttc gtc tcc atg cag gcc atg ata gat gcg Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala	288
85 90 95	
atg gac cgg ctg cag atc ccc ttc agc agg cct gac agc aag cag cac Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His	336
100 105 110	
gcc agc cta gtg atg acc cag gac ccc tat aaa gtg agc aca ttc gag Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu	384
115 120 125	
aag cca tat gca gtg gcc atg cag tac ctg tgg cgg gac gcg ggc atc Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile	432
130 135 140	
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145 150 155 160	
gtg tat tac ctg tca cac ctg gag cgc ata tca gag gac agc tac atc Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile	528
165 170 175	
ccc act gcg caa gac gtg ctg cgc agt cgc atg ccc acc aca ggc atc Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile	576
180 185 190	
aat gag tac tgc ttc tcc gtg aag aaa acc aaa ctg cgc atc gtg gat Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp	624
195 200 205	
gtt ggt ggc cag agg tca gag cgt agg aaa tgg att cac tgt ttc gag Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu	672
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aac gtg att gcc ctc atc tac ctg gcc tcc ctg agc gag tat gac cag Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln	720
225 230 235 240	
tgc cta gag gag aac gat cag gag aac cgc atg gag gag agt ctc gct Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala	768
245 250 255	
ctg ttc agc acg atc cta gag ctg ccc tgg ttc aag agc acc tcg gtc Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val	816
260 265 270	
atc ctc ttc ctc aac aag acg gac atc ctg gaa gat aag att cac acc Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr	864
275 280 285	
tcc cac ctg gcc aca tac ttc ccc agc ttc cag gga ccc cgg cga gac Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp	912
290 295 300	

gca gag gcc gcc aag agc ttc atc ttg gac atg tat gcg cgc gtg tac 960  
 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr 320  
 305 310 315

gcg agc tgc gca gag ccc cag gac ggt ggc agg aaa ggc tcc cgc gcg 1008  
 Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala 335  
 325 330

cgc cgc ttc ttc gca cac ttc acc tgt gcc acg gac acg caa agc gtc 1056  
 Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val 350  
 340 345

cgc agc gtg ttc aag gac gtg cgg gac tcg gtg ctg gcc cgg tac ctg 1104  
 Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu 365  
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gac gag atc aac ctg ctg tga 1125  
 Asp Glu Ile Asn Leu Leu 370

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 Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu  
 35 40 45  
 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile  
 50 55 60  
 Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Ala Phe Arg Leu  
 65 70 75 80  
 Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala  
 85 90 95  
 Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His  
 100 105 110  
 Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu  
 115 120 125  
 Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile  
 130 135 140  
 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala  
 145 150 155 160  
 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile  
 165 170 175  
 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile  
 180 185 190  
 Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp  
 195 200 205  
 Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu  
 210 215 220  
 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln  
 225 230 235 240  
 Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala  
 245 250 255  
 Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val  
 260 265 270  
 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr  
 275 280 285  
 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp  
 290 295 300  
 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr  
 305 310 315 320

Ala	Ser	Cys	Ala	Glu	Pro	Gln	Asp	Gly	Gly	Arg	Lys	Gly	Ser	Arg	Ala
				325					330					335	
Arg	Arg	Phe	Phe	Ala	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr	Gln	Ser	Val
			340					345					350		
Arg	Ser	Val	Phe	Lys	Asp	Val	Arg	Asp	Ser	Val	Leu	Ala	Arg	Tyr	Leu
		355					360					365			
Asp	Glu	Ile	Asn	Leu	Leu										
	370														

# SEQUENCE ID LISTING

## Nucleotide and Amino Acid Sequences of Gα15

(SEQ ID NO: 2 and SEQ ID NO: 4, respectively)

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Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu Glu Glu					
63	72	81	90	99	108
AAG ACT GCC GCC AGA ATC GAC CAG GAG ATC AAC AGG ATT TTG TTG GAA CAG AAA					
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Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu Leu Glu Gln Lys					
117	126	135	144	153	162
AAA CAA GAG CGC GAG GAA TTG AAA CTC CTG CTG TTG GGG CCT GGT GAG AGC GGG					
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Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu Gly Pro Gly Glu Ser Gly					
171	180	189	198	207	216
AAG AGT ACG TTC ATC AAG CAG ATG CGC ATC ATT CAC GGT GTG GGC TAC TCG GAG					
-----					
Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Val Gly Tyr Ser Glu					
225	234	243	252	261	270
GAG GAC CGC AGA GCC TTC CGG CTG CTC ATC TAC CAG AAC ATC TTC GTC TCC ATG					
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Glu Asp Arg Arg Ala Phe Arg Leu Leu Ile Tyr Gln Asn Ile Phe Val Ser Met					

279	288	297	306	315	324
CAG GCC ATG ATA GAT GCG ATG GAC CGG CTG CAG ATC CCC TTC AGC AGG CCT GAC					
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Gln Ala Met Ile Asp Ala Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp					
333	342	351	360	369	378
AGC AAG CAG CAC GCC AGC CTA GTG ATG ACC CAG GAC CCC TAT AAA GTG AGC ACA					
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Ser Lys Gln His Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr					
387	396	405	414	423	432
TTC GAG AAG CCA TAT GCA GTG GCC ATG CAG TAC CTG TGG CGG GAC GCG GGC ATC					
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Phe Glu Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile					
441	450	459	468	477	486
CGT GCA TGC TAC GAG CGA AGG CGT GAA TTC CAC CTT CTG GAC TCC GCG GTG TAT					
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Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr					
495	504	513	522	531	540
TAC CTG TCA CAC CTG GAG CGC ATA TCA GAG GAC AGC TAC ATC CCC ACT GCG CAA					
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Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile Pro Thr Ala Gln					
549	558	567	576	585	594
GAC GTG CTG CGC AGT CGC ATG CCC ACC ACA GGC ATC AAT GAG TAC TGC TTC TCC					
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Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile Asn Glu Tyr Cys Phe Ser					
603	612	621	630	639	648
GTG AAG AAA ACC AAA CTG CGC ATC GTG GAT GTT GGT GGC CAG AGG TCA GAG CGT					
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Val Lys Lys Thr Lys Leu Arg Ile Val Asp Val Gly Gly Gln Arg Ser Glu Arg					



657	666	675	684	693	702
AGG AAA TGG ATT CAC TGT TTC GAG AAC GTG ATT GCC CTC ATC TAC CTG GCC TCC					
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Arg Lys Trp Ile His Cys Phe Glu Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser					
711	720	729	738	747	756
CTG AGC GAG TAT GAC CAG TGC CTA GAG GAG AAC GAT CAG GAG AAC CGC ATG GAG					
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Leu Ser Glu Tyr Asp Gln Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu					
765	774	783	792	801	810
GAG AGT CTC GCT CTG TTC AGC ACG ATC CTA GAG CTG CCC TGG TTC AAG AGC ACC					
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Glu Ser Leu Ala Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr					
819	828	837	846	855	864
TCG GTC ATC CTC TTC CTC AAC AAG ACG GAC ATC CTG GAA GAT AAG ATT CAC ACC					
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Ser Val Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr					
873	882	891	900	909	918
TCC CAC CTG GCC ACA TAC TTC CCC AGC TTC CAG GGA CCC CGG CGA GAC GCA GAG					
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Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp Ala Glu					
927	936	945	954	963	972
GCC GCC AAG AGC TTC ATC TTG GAC ATG TAT GCG CGC GTG TAC GCG AGC TGC GCA					
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Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr Ala Ser Cys Ala					
981	990	999	1008	1017	1026
GAG CCC CAG GAC GGT GGC AGG AAA GGC TCC CGC GCG CGC CGC TTC TTC GCA CAC					
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Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala Arg Arg Phe Phe Ala His					

1035	1044	1053	1062	1071	1080
TTC ACC TGT GCC ACG GAC ACG CAA AGC GTC CGC AGC GTG TTC AAG GAC GTG CGG					
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Phe Thr Cys Ala Thr Asp Thr Gln Ser Val Arg Ser Val Phe Lys Asp Val Arg					

  

1089	1098	1107	1116	1125
GAC TCG GTG CTG GCC CGG TAC CTG GAC GAG ATC AAC CTG CTG TGA				
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Asp Ser Val Leu Ala Arg Tyr Leu Asp Glu Ile Asn Leu Leu ***				

Nucleotide and Amino Acid Sequences of G 16  
(SEQ ID NO: 1 and SEQ ID NO: 3, respectively)

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Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu Asp Glu					

  

63	72	81	90	99	108
AAG GCC GCC GCC CGG GTG GAC CAG GAG ATC AAC AGG ATC CTC TTG GAG CAG AAG					
----					
Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu Leu Glu Gln Lys					

  

117	126	135	144	153	162
AAG CAG GAC CGC GGG GAG CTG AAG CTG CTG CTT TTG GGC CCA GGC GAG AGC GGG					
----					
Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu Gly Pro Gly Glu Ser Gly					

  

171	180	189	198	207	216
AAG AGC ACC TTC ATC AAG CAG ATG CGG ATC ATC CAC GGC GCC GGC TAC TCG GAG					
----					
Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ala Gly Tyr Ser Glu					

  

225	234	243	252	261	270
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GAG GAG CGC AAG GGC TTC CGG CCC CTG GTC TAC CAG AAC ATC TTC GTG TCC ATG  
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 Glu Glu Arg Lys Gly Phe Arg Pro Leu Val Tyr Gln Asn Ile Phe Val Ser Met

279 288 297 306 315 324  
 CGG GCC ATG ATC GAG GCC ATG GAG CGG CTG CAG ATT CCA TTC AGC AGG CCC GAG  
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 Arg Ala Met Ile Glu Ala Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu

333 342 351 360 369 378  
 AGC AAG CAC CAC GCT AGC CTG GTC ATG AGC CAG GAC CCC TAT AAA GTG ACC ACG  
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 Ser Lys His His Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr

387 396 405 414 423 432  
 TTT GAG AAG CGC TAC GCT GCG GCC ATG CAG TGG CTG TGG AGG GAT GCC GGC ATC  
 ---  
 Phe Glu Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile

441 450 459 468 477 486  
 CGG GCC TGC TAT GAG CGT CGG CGG GAA TTC CAC CTG CTC GAT TCA GCC GTG TAC  
 ---  
 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr

495 504 513 522 531 540  
 TAC CTG TCC CAC CTG GAG CGC ATC ACC GAG GAG GGC TAC GTC CCC ACA GCT CAG  
 ---  
 Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val Pro Thr Ala Gln

549 558 567 576 585 594  
 GAC GTG CTC CGC AGC CGC ATG CCC ACC ACT GGC ATC AAC GAG TAC TGC TTC TCC  
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 Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile Asn Glu Tyr Cys Phe Ser

603 612 621 630 639 648  
 GTG CAG AAA ACC AAC CTG CGG ATC GTG GAC GTC GGG GGC CAG AAG TCA GAG CGT

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Val Gln Lys Thr Asn Leu Arg Ile Val Asp Val Gly Gly Gln Lys Ser Glu Arg

657 666 675 684 693 702  
AAG AAA TGG ATC CAT TGT TTC GAG AAC GTG ATC GCC CTC ATC TAC CTG GCC TCA

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Lys Lys Trp Ile His Cys Phe Glu Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser

711 720 729 738 747 756  
CTG AGT GAA TAC GAC CAG TGC CTG GAG GAG AAC AAC CAG GAG AAC CGC ATG AAG

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Leu Ser Glu Tyr Asp Gln Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys

765 774 783 792 801 810  
GAG AGC CTC GCA TTG TTT GGG ACT ATC CTG GAA CTA CCC TGG TTC AAA AGC ACA

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Glu Ser Leu Ala Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr

819 828 837 846 855 864  
TCC GTC ATC CTC TTT CTC AAC AAA ACC GAC ATC CTG GAG GAG AAA ATC CCC ACC

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Ser Val Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr

873 882 891 900 909 918  
TCC CAC CTG GCT ACC TAT TTC CCC AGT TTC CAG GGC CCT AAG CAG GAT GCT GAG

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Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp Ala Glu

927 936 945 954 963 972  
GCA GCC AAG AGG TTC ATC CTG GAC ATG TAC ACG AGG ATG TAC ACC GGG TGC GTG

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Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr Thr Gly Cys Val

981 990 999 1008 1017 1026  
GAC GGC CCC GAG GGC AGC AAG AAG GGC GCA CGA TCC CGA CGC CTT TTC AGC CAC

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Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser Arg Arg Leu Phe Ser His

1035	1044	1053	1062	1071	1080												
TAC	ACA	TGT	GCC	ACA	GAC	ACA	CAG	AAC	ATC	CGC	AAG	GTC	TTC	AAG	GAC	GTG	CGG
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Tyr	Thr	Cys	Ala	Thr	Asp	Thr	Gln	Asn	Ile	Arg	Lys	Val	Phe	Lys	Asp	Val	Arg

1035  
 1044  
 1053  
 1062  
 1071  
 1080

1089	1098	1107	1116	1125										
GAC	TCG	GTG	CTC	GCC	CGC	TAC	CTG	GAC	GAG	ATC	AAC	CTG	CTG	TGA
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Asp	Ser	Val	Leu	Ala	Arg	Tyr	Leu	Asp	Glu	Ile	Asn	Leu	Leu	***